

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 9, 2006, 15:43:08 ; Search time 33 Seconds

(without alignments)  
34.676 Million cell updates/sec

Title: US-10-810-919-4

Sequence: 1 VHQKLPFAEDVGSNK 17

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 6712017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum March 0%

Maximum March 100%  
Listing first 1000 summaries

Database:

Published Applications AA New:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	84	90.3	40	7	US-11-104-300-3
6	84	90.3	40	7	US-11-269-857-3
7	84	90.3	42	1	US-09-731-899-3
8	84	90.3	42	6	US-10-890-071-42
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28	77	82.8	42	6	US-10-515-919A-11	Sequence 11, Appl1
29	77	82.8	62	6	US-10-515-919A-14	Sequence 14, Appl1
30	77	82.8	62	6	US-10-515-919A-16	Sequence 16, Appl1
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35	76	81.7	62	6	US-10-515-919A-12	Sequence 12, Appl1
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OM protein - protein search, using sw model

Run on: August 9, 2006, 15:42:02 ; Search time 183 Seconds  
(without alignments)  
43.031 Million cell updates/sec

Title: US-10-810-919-4  
Perfect score: 93  
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Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 1000 summaries

Database : Published Applications MA Main:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	100	17	US-10-810-919-4	Sequence 4, Appl1
2	84	90.3	17	US-09-998-491-8	Sequence 8, Appl1
3	84	90.3	17	US-10-475-281-8	Sequence 8, Appl1
4	84	90.3	17	US-10-810-919-3	Sequence 3, Appl1
5	84	90.3	17	US-10-684-346-24	Sequence 26, Appl1
6	84	90.3	17	US-10-997-078-46	Sequence 46, Appl1
7	84	90.3	17	US-10-997-700-19	Sequence 19, Appl1
8	84	90.3	17	US-11-066-697-950	Sequence 950, App
9	84	90.3	17	US-11-066-697-983	Sequence 983, App
10	84	90.3	24	US-10-728-246-5	Sequence 5, Appl1
11	84	90.3	24	US-11-030-300-5	Sequence 5, Appl1
12	84	90.3	28	US-09-867-847-4	Sequence 4, Appl1
13	84	90.3	28	US-09-865-294-66	Sequence 66, Appl1
14	84	90.3	28	US-09-792-079-5	Sequence 5, Appl1
15	84	90.3	28	US-10-159-279-5	Sequence 5, Appl1
16	84	90.3	28	US-10-363-082-2	Sequence 2, Appl1
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18	84	90.3	28	US-10-350-472-4	Sequence 4, Appl1
19	84	90.3	28	US-10-741-205-36	Sequence 36, Appl1
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21	84	90.3	28	US-10-478-308-4	Sequence 4, Appl1
22	84	90.3	28	US-10-478-307-4	Sequence 4, Appl1
23	84	90.3	28	US-10-861-614-66	Sequence 66, Appl1
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145	84	90.3	42	3	US-09-865-294-65	Sequence 65, Appl1	218	84	90.3	42	5	US-10-852-850-1	Sequence 1, Appl1
146	84	90.3	42	3	US-09-792-079-13	Sequence 13, Appl1	219	84	90.3	42	5	US-10-830-271-42	Sequence 42, Appl1
147	84	90.3	42	3	US-09-825-242-1	Sequence 1, Appl1	220	84	90.3	42	5	US-10-903-679-1	Sequence 1, Appl1
148	84	90.3	42	3	US-09-930-915A-293	Sequence 293, App	221	84	90.3	42	5	US-10-810-881A-50	Sequence 50, Appl1
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151	84	90.3	42	4	US-10-217-584-2	Sequence 2, Appl1	224	84	90.3	42	5	US-10-508-586-1	Sequence 1, Appl1
152	84	90.3	42	4	US-10-169-580-2	Sequence 2, Appl1	225	84	90.3	42	5	US-10-505-513-27	Sequence 27, Appl1
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154	84	90.3	42	4	US-10-143-534-2	Sequence 2, Appl1	227	84	90.3	42	5	US-10-923-267-1	Sequence 1, Appl1
155	84	90.3	42	4	US-10-190-548A-1	Sequence 1, Appl1	228	84	90.3	42	5	US-10-928-926-42	Sequence 42, Appl1
156	84	90.3	42	4	US-10-051-663-2	Sequence 2, Appl1	229	84	90.3	42	5	US-10-923-605-1	Sequence 1, Appl1
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158	84	90.3	42	4	US-10-050-902-220	Sequence 220, App	231	84	90.3	42	5	US-10-945-751-157	Sequence 157, App
159	84	90.3	42	4	US-10-050-898-220	Sequence 220, App	232	84	90.3	42	5	US-10-945-133-1	Sequence 1, Appl1
160	84	90.3	42	4	US-10-082-014-81	Sequence 81, Appl1	233	84	90.3	42	5	US-10-966-9198-3	Sequence 3, Appl1
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163	84	90.3	42	4	US-10-231-298B-15	Sequence 15, Appl1	236	84	90.3	42	6	US-11-007-643-37	Sequence 37, Appl1
164	84	90.3	42	4	US-10-231-470C-15	Sequence 15, Appl1	237	84	90.3	42	6	US-11-007-644-37	Sequence 37, Appl1
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166	84	90.3	42	4	US-10-366-125-98	Sequence 28, Appl1	239	84	90.3	42	6	US-11-021-951-190	Sequence 190, App
167	84	90.3	42	4	US-10-431-544-2	Sequence 2, Appl1	240	84	90.3	42	6	US-11-091-309-2	Sequence 2, Appl1
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170	84	90.3	42	4	US-10-337-261-2	Sequence 2, Appl1	243	84	90.3	42	6	US-11-016-706-37	Sequence 37, Appl1
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OW protein - protein search, using sw model

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29.760 Million cell updates/sec

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Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

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Post-processing: Minimum Match 0%  
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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	90.3	17	US-09-264-709A-2	Sequence 2, Appli
2	84	90.3	17	US-09-623-548A-950	Sequence 950, App
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5	84	90.3	17	US-09-657-276-950	Sequence 983, App
6	84	90.3	26	US-08-304-585-7	Sequence 7, Appli
7	84	90.3	28	US-08-346-849-4	Sequence 4, Appli
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10	84	90.3	28	US-08-986-948-7	Sequence 2, Appli
11	84	90.3	28	US-08-293-284A-4	Sequence 4, Appli
12	84	90.3	28	US-08-461-216-2	Sequence 2, Appli
13	84	90.3	28	US-09-388-890-2	Sequence 2, Appli
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31	84	90.3	28	US-09-623-548A-959	Sequence 959, App
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34	84	90.3	28	US-09-623-548A-992	Sequence 992, App
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38	84	90.3	28	US-09-657-276-976	Sequence 976, App
39	84	90.3	28	US-09-657-276-992	Sequence 992, App
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46	84	90.3	35	US-08-304-585-6	Sequence 6, Appli
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124	84	90.3	42	2	US-09-660-954-1	Sequence 2, Appli	197	84	90.3	43	2	US-09-481-980A-1	Sequence 1, Appli
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137	84	90.3	42	2	US-09-723-762-1	Sequence 1, Appli	210	84	90.3	43	2	US-09-623-548A-954	Sequence 954, App
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139	84	90.3	42	2	US-09-724-551-42	Sequence 42, Appli	212	84	90.3	43	2	US-09-992-800-1	Sequence 1, Appli
140	84	90.3	42	2	US-10-815-353-1	Sequence 1, Appli	213	84	90.3	43	2	US-09-657-776-954	Sequence 954, App
141	84	90.3	42	2	US-10-278-181-1	Sequence 1, Appli	214	84	90.3	43	2	US-09-657-776-987	Sequence 1, Appli
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146	84	90.3	42	2	US-09-724-953-34	Sequence 34, Appli	219	84	90.3	47	1	US-08-609-090-10	Sequence 10, Appli
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153	84	90.3	42	2	US-09-585-817-34	Sequence 34, Appli	226	84	90.3	59	1	US-08-484-969-3	Sequence 3, Appli
154	84	90.3	42	2	US-09-962-955D-37	Sequence 37, Appli	227	84	90.3	59	1	US-08-472-627-3	Sequence 3, Appli
155	84	90.3	42	2	US-09-706-574A-20	Sequence 20, Appli	228	84	90.3	59	1	US-08-388-463-3	Sequence 3, Appli
156	84	90.3	42	2	US-10-934-609-1	Sequence 1, Appli	229	84	90.3	63	1	US-08-462-859A-4	Sequence 4, Appli
157	84	90.3	42	2	US-10-884-892-1	Sequence 1, Appli	230	84	90.3	63	1	US-08-123-659A-4	Sequence 4, Appli
158	84	90.3	42	2	US-09-848-616-174	Sequence 174, App	231	84	90.3	63	1	US-08-464-247A-4	Sequence 4, Appli
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160	84	90.3	42	2	US-10-815-404-1	Sequence 1, Appli	233	84	90.3	67	2	US-09-027-258-1	Sequence 1, Appli
161	84	90.3	42	2	US-10-816-380-1	Sequence 1, Appli	234	84	90.3	70	3	US-09-155-076-14	Sequence 14, Appli
162	84	90.3	42	3	US-10-363-082-1	Sequence 1, Appli	235	84	90.3	82	2	US-09-848-616-173	Sequence 173, App
163	84	90.3	42	3	US-10-363-082-1	Sequence 1, Appli	236	84	90.3	82	7	5187153-8	Patent No. 5187153
164	84	90.3	42	5	PCT-US92-06700-2	Sequence 2, Appli	237	84	90.3	97	7	5220013-8	Patent No. 5220013
165	84	90.3	42	5	PCT-US93-00325-1	Sequence 1, Appli	238	84	90.3	97	7	5223482-8	Patent No. 5223482
166	84	90.3	42	7	5220013-14	Patent No. 5220013	239	84	90.3	99	2	US-08-422-333-3	Sequence 3, Appli
167	84	90.3	43	1	US-08-235-400-1	Sequence 1, Appli	240	84	90.3	99	2	US-08-339-708A-4	Sequence 8, Appli
168	84	90.3	43	1	US-08-437-067-1	Sequence 1, Appli	241	84	90.3	99	2	US-08-339-708A-8	Sequence 8, Appli
169	84	90.3	43	1	US-08-302-808-6	Sequence 6, Appli	242	84	90.3	100	7	5187153-10	Patent No. 5187153
170	84	90.3	43	1	US-08-079-511-1	Sequence 1, Appli	243	84	90.3	100	7	5220013-10	Patent No. 5220013
171	84	90.3	43	1	US-08-467-607-1	Sequence 1, Appli	244	84	90.3	100	7	5223482-10	Patent No. 5223482
172	84	90.3	43	1	US-08-404-831-1	Sequence 1, Appli	245	84	90.3	103	1	US-08-404-831-2	Sequence 2, Appli

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OM protein - protein search, using sw model

Run on: August 9, 2006, 15:32:27 ; Search time 299 Seconds  
(without alignments)  
52.593 Million cell updates/sec

Title: US-10-810-919-4

Perfect score: 93  
Sequence: 1 VHHQKLPFAEDVGSNK 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : UniProt 7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	90.3	33	09UC33_HUMAN	Q9UC33 homo sapien
2	84	90.3	42	056J36_GRAIR	Q56J36 girapua gri
3	84	90.3	42	056J37_TUTER	Q56J37 turapua tr
4	84	90.3	42	07M088_CANPO	Q7M088 cavia porce
5	84	90.3	52	08W299_HUMAN	Q8W299 homo sapien
6	84	90.3	57	A4_CANFA	Q29149 u amyloid b
7	84	90.3	58	A4_URGMA	Q28280 c amyloid b
8	84	90.3	58	A4_RABIT	Q28748 o amyloid b
9	84	90.3	58	A4_SHEEP	Q28757 o amyloid b
10	84	90.3	59	A4_BOVIN	Q28053 b amyloid b
11	84	90.3	113	08UH58_CHESE	Q8UH58 chelydra se
12	84	90.3	534	093296_CHICK	Q93296 gallus gall
13	84	90.3	569	09PV11_CHICK	Q9PV11 gallus gall
14	84	90.3	695	02XOAO_PIG	Q2XOAO sus scrofa
15	84	90.3	695	056J33_CANFA	Q56J33 canis faml
16	84	90.3	695	05R477_PONPY	Q5R477 pongo pygma
17	84	90.3	695	06RH28_CANFA	Q6RH28 canis faml
18	84	90.3	695	09DGJ6_CHICK	Q9DGJ6 gallus gall
19	84	90.3	714	056J34_CANFA	Q56J34 canis faml
20	84	90.3	749	056J32_STECO	Q56J32 strella co
21	84	90.3	751	A4_SATSC	Q95241 s amyloid b
22	84	90.3	751	06GSC0_HUMAN	Q6GSC0 homo sapien
23	84	90.3	751	04R4R8_MACFA	Q4R4R8 macaca fasc
24	84	90.3	751	056J35_CANFA	Q56J35 canis faml
25	84	90.3	751	06RH28_CANFA	Q6RH28 canis faml
26	84	90.3	751	02XO99_PIG	Q2XO99 sus scrofa
27	84	90.3	751	09DGJ7_CHICK	Q9DGJ7 gallus gall
28	84	90.3	754	04RYJ3_TETNG	Q4RYJ3 tetraodon n
29	84	90.3	770	A4_CAVFO	Q05067 h amyloid b
30	84	90.3	770	A4_HUMAN	P53601 m amyloid b
31	84	90.3	770	A4_MACFA	P53601 m amyloid b

32	84	90.3	770	1	A4_PANTR	Q51680 p amyloid b
33	84	90.3	770	1	A4_PIG	P79307 s amyloid b
34	84	90.3	770	2	056J36_CANFA	Q56J36 canis faml
35	84	90.3	770	2	06RH30_CANFA	Q6RH30 canis faml
36	84	90.3	780	1	A4_TETFL	Q73683 tetraodon t
37	84	90.3	780	1	098SG0_XENLA	Q98SG0 xenopus lae
38	84	90.3	780	1	091963_PIPPI	Q91963 xenopus ap
39	84	90.3	780	1	06NRRI_XENLA	Q6NRRI xenopus lae
40	84	90.3	780	1	06DJBE_XENTR	Q6DJBE xenopus lae
41	84	90.3	780	1	07ZXQ0_XENLA	Q7ZXQ0 xenopus lae
42	84	90.3	780	1	098819_XENOPUS	Q98819 xenopus lae
43	84	90.3	780	1	035463_CRIGR	Q35463 cricetus
44	84	90.3	780	1	08BPV5_MOUSE	Q8BPV5 mus musculu
45	84	90.3	780	1	08BPC7_MOUSE	Q8BPC7 mus musculu
46	84	90.3	780	1	06GR78_MOUSE	Q6GR78 mus musculu
47	84	90.3	780	1	06R6Q5_PAT	Q6R6Q5 ratcus norv
48	84	90.3	780	1	03TWI3_MOUSE	Q3TWI3 mus musculu
49	84	90.3	780	1	03TXI9_MOUSE	Q3TXI9 mus musculu
50	84	90.3	780	1	A4_MOUSE	P12023 m amyloid b
51	84	90.3	780	1	A4_RAT	P08592 r amyloid b
52	84	90.3	780	1	053ZT3_MOUSE	Q53ZT3 mus musculu
53	84	90.3	780	1	0547B7_PAT	Q547B7 ratcus norv
54	84	90.3	780	1	03WQ25_ANTST	Q3WQ25 antechinus
55	84	90.3	780	1	057394_NARJA	Q57394 narke japon
56	84	90.3	780	1	A4_FUGRU	Q93279 fugu rubrip
57	84	90.3	780	1	04S04_TETNG	Q4S04 tetraodon n
58	84	90.3	780	1	08UUR8_BRARE	Q8UUR8 brachydanio
59	84	90.3	780	1	08UUS0_BRARE	Q8UUS0 brachydanio
60	84	90.3	780	1	0919E7_BRARE	Q919E7 brachydanio
61	84	90.3	780	1	07ZET1_BRARE	Q7ZET1 brachydanio
62	84	90.3	780	1	06NUZ1_BRARE	Q6NUZ1 brachydanio
63	84	90.3	780	1	090WZ8_BRARE	Q90WZ8 brachydanio
64	84	90.3	780	1	097917_BOVIN	Q97917 bos taurus
65	84	90.3	780	1	02XO96_PIG	Q2XO96 sus scrofa
66	84	90.3	780	1	08UUI7_BRARE	Q8UUI7 brachydanio
67	84	90.3	780	1	05XIV5_BRARE	Q5XIV5 brachydanio
68	84	90.3	780	1	08UUR9_BRARE	Q8UUR9 brachydanio
69	84	90.3	780	1	094LB4_ORYSA	Q94LB4 oryza sativ
70	84	90.3	780	1	0815V7_ARATH	Q815V7 arabidopsis
71	84	90.3	780	1	09M1K5_ARATH	Q9M1K5 arabidopsis
72	84	90.3	780	1	056DL4_ROWMI	Q56DL4 romalea mic
73	84	90.3	780	1	06BM96_DEBHA	Q6BM96 debaryomyce
74	84	90.3	780	1	04DWK3_TRYCR	Q4DWK3 trypanosoma
75	84	90.3	780	1	04E557_TRYCR	Q4E557 trypanosoma
76	84	90.3	780	1	03OR64_THIND	Q3OR64 thiomicrosp
77	84	90.3	780	1	05C081_SCHUA	Q5C081 schistosoma
78	84	90.3	780	1	08XOM0_NEUCR	Q8XOM0 neurospora
79	84	90.3	780	1	09USK4_SPOLT	Q9USK4 spodoptera
80	84	90.3	780	1	P11_BUCBP	Q89B04 buchnera ap
81	84	90.3	780	1	03YUJ3_BIOGL	Q3YUJ3 biophalaris
82	84	90.3	780	1	09K6M6_BACHD	Q9K6M6 bacillus ha
83	84	90.3	780	1	Q4IBK7_GIBZE	Q4IBK7 gibberella
84	84	90.3	780	1	Q4IR56_GIBZE	Q4IR56 gibberella
85	84	90.3	780	1	06J4Q1_APIME	Q6J4Q1 apis mellif
86	84	90.3	780	1	09GYW1_AEDAS	Q9GYW1 aedes aegypt
87	84	90.3	780	1	09N2P8_DIPPT	Q9N2P8 anopheles g
88	84	90.3	780	1	09GYW2_AEDAS	Q9GYW2 aedes aegypt
89	84	90.3	780	1	Q4I728_GIBZE	Q4I728 gibberella
90	84	90.3	780	1	Q3EGP5_ACTBSC	Q3EGP5 actinobacill
91	84	90.3	780	1	Q3VY94_YACTO	Q3VY94 frankia sp.
92	84	90.3	780	1	Q3XCS3_ALTAT	Q3XCS3 pseudalter
93	84	90.3	780	1	Q7VOY1_BLOFL	Q7VOY1 blochmannia
94	84	90.3	780	1	HCYE_EURCA	P02232 euryptera c
95	84	90.3	780	1	Q7Q7X0_ANOGA	Q7Q7X0 anopheles g
96	84	90.3	780	1	08MZM4_ANOGA	Q8MZM4 anopheles g
97	84	90.3	780	1	SSP2_BOOMO	P20613 bombyx mori
98	84	90.3	780	1	Q7PUB0_ANOGA	Q7PUB0 anopheles g
99	84	90.3	780	1	Q44BM0_CHILI	Q44BM0 chlorobium
100	84	90.3	780	1	06BMO0_DBBHA	Q6BMO0 debaryomyce
101	84	90.3	780	1	Q9GKT8_MACFA	Q9GKT8 macaca fasc
102	84	90.3	780	1	Q3ZK57_GREOV	Q3ZK57 human rolav
103	84	90.3	780	1	Q5OR08_ENTHI	Q5OR08 entameba h
104	84	90.3	780	1	Q3VOM3_MOUSE	Q3VOM3 mus musculu



105	43	45.2	227	2	05P072_XENTLA	05P072_xenopus lae	178	42	45.2	690	2	09V896_DROME	09V896_drosophila
106	43	45.2	229	2	05B2A7_SCHUA	05B2A7_bacilosoma	179	42	45.2	749	2	04ANR6_SCHLB	04ANR6_schlotheimia
107	43	45.2	251	2	09ZKR7_HELPJ	09ZKR7_helpj	180	42	45.2	751	2	04XU14_PLACH	04XU14_plach
108	43	45.2	308	2	08A206_BACTN	08A206_bacteroides	181	42	45.2	831	2	07VNB0_HAEDU	07VNB0_haemophilus
109	43	45.2	320	2	058KH0_9BACT	058KH0_leptospirillum	182	42	45.2	856	2	09V706_DROME	09V706_drosophila
110	43	45.2	344	2	08G8J0_ERMPY	08G8J0_erythroneura	183	42	45.2	856	2	02Q200_ORYSA	02Q200_oryza sativa
111	43	45.2	352	2	07M7X9_MOLSU	07M7X9_molophilus	184	42	45.2	909	2	07O1V6_ANOGA	07O1V6_anopheles
112	43	45.2	395	2	08X0K3_NEUCR	08X0K3_neurospora	185	42	45.2	1080	1	HDC_DROME	HDC_drosophila
113	43	45.2	500	2	07V6G0_HELHP	07V6G0_helicobacter	186	42	45.2	1576	2	03KN39_DROME	03KN39_drosophila
114	43	45.2	578	2	0613E7_CAEBC	0613E7_caenorhabditis	187	42	44.6	173	2	03N6V2_9PROT	03N6V2_nitrosomonas
115	43	45.2	626	2	086N90_9ARAC	086N90_nephila hna	188	41	44.1	192	2	07YVP8_9TRYP	07YVP8_trypanosoma
116	43	45.2	628	1	HCYC_EURCA	09F15_eurypelma c	189	41	44.1	125	2	08CSRS_STAES	08CSRS_staphylococcus
117	43	45.2	628	1	HCYC_EURCA	09F15_eurypelma c	190	41	44.1	183	2	075FRO_LEPIC	075FRO_leptospira
118	43	45.2	632	2	07PX17_ANOGA	07PX17_anopheles g	191	41	44.1	183	2	08EXR3_LEPIN	08EXR3_leptospira
119	43	45.2	638	2	0580B6_9TRYP	0580B6_trypanosoma	192	41	44.1	188	2	03C0S5_ALTAT	03C0S5_pseudalter
120	43	45.2	687	2	09GYX9_9DIPT	09GYX9_arnigera s	193	41	44.1	194	2	05GJ05_PENUP	05GJ05_penaeus jap
121	43	45.2	689	2	P90664_AEDAE	P90664_aedes aegypti	194	41	44.1	194	2	082LNI1_STRAW	082LNI1_streptomyces
122	43	45.2	690	2	022464_9GAMM	022464_shevanella	195	41	44.1	195	2	04JUV7_CORUK	04JUV7_corynebacter
123	43	45.2	690	2	035UT4_9GAMM	035UT4_shevanella	196	41	44.1	213	2	093WV1_9STRE	093WV1_streptococcus
124	43	45.2	690	2	0355G3_9GAMM	0355G3_shevanella	197	41	44.1	229	2	09MCQ2_BPD3	09MCQ2_bacteriophages
125	43	45.2	690	2	030337_9GAMM	030337_shevanella	198	41	44.1	240	1	ZERA_MATZE	ZERA_matsche
126	43	45.2	690	2	08EFZ5_SHEON	08EFZ5_shevanella	199	41	44.1	241	2	0946V7_MATZE	0946V7_zea mays (m
127	43	45.2	700	2	07P101_ANOGA	07P101_anopheles g	200	41	44.1	251	2	0413H5_GIBZE	0413H5_gibberella
128	43	45.2	700	2	08WMZ3_ANOGA	08WMZ3_anopheles g	201	41	44.1	253	2	03QGL2_9GAMM	03QGL2_pseudomonas
129	43	45.2	703	1	ARYB_MANSR	P14297_manduca sex	202	41	44.1	258	2	08VMS1_9PSED	08VMS1_pseudomonas
130	43	45.2	704	1	ARY_NANPE	07A1F8_antheraea p	203	41	44.1	287	2	05SWU4_MOUSE	05SWU4_mus musculus
131	43	45.2	711	2	04P0X3_USTMA	04P0X3_ustuligo ma	204	41	44.1	290	2	05QR21_MOUSE	05QR21_mus musculus
132	43	45.2	739	2	03VM70_9CLHB	03VM70_pelodictyon	205	41	44.1	296	2	07VZH2_BORPE	07VZH2_bordeletia
133	43	45.2	779	2	09KPM3_VIBCH	09KPM3_vibrio chol	206	41	44.1	303	2	02VJ86_9ENTR	02VJ86_erythrocyte
134	43	45.2	920	2	04R9T4_TERNG	04R9T4_tetradon n	207	41	44.1	301	2	07WGB5_BORBR	07WGB5_bordeletia
135	43	45.2	1749	2	07RNGH_PLAYO	07RNGH_plasmodium	208	41	44.1	308	2	04RRP5_TETNG	04RRP5_tetradon n
136	43	45.2	2238	2	054S11_DICDI	054S11_dicystosteli	209	41	44.1	320	2	0916V5_PSEAE	0916V5_pseudomonas
137	43	45.2	186	2	034V06_9GAMM	034V06_alkaliphilum	210	41	44.1	341	1	MORB_HAET8	MORB_haemophilus
138	43	45.2	368	2	0861M1_DICDI	0861M1_dicystosteli	211	41	44.1	355	2	06M174_METWP	06M174_methanococcus
139	43	45.2	395	2	055923_DICDI	055923_dicystosteli	212	41	44.1	376	2	076EX8_SOYBN	076EX8_glycine max
140	43	45.2	771	2	041J39_GIBZE	041J39_gibberella	213	41	44.1	376	2	084X84_SOYBN	084X84_glycine max
141	42.5	45.7	1740	2	06ENK5_ORYSA	06ENK5_oryza sativa	214	41	44.1	380	1	FAD33_SOYBN	FAD33_glycine max
142	42	45.2	162	2	02MUV9_CIOBE	02MUV9_clostridium	215	41	44.1	380	2	05CDB3_SOYBN	05CDB3_glycine max
143	42	45.2	211	1	HAWI_BRAVA	089WXS_bradynothob	216	41	44.1	380	2	084X83_SOYBN	084X83_glycine max
144	42	45.2	245	2	05A406_CANAL	05A406_candida alb	217	41	44.1	388	2	031SH9_NATPD	031SH9_nectomonas
145	42	45.2	318	2	03AL13_SYNSC	03AL13_synochococc	218	41	44.1	390	2	09KCE3_BACHD	09KCE3_bacillus ha
146	42	45.2	337	2	09GV29_DROME	09GV29_drosophila	219	41	44.1	427	2	02U629_ASPPOR	02U629_aspergillus
147	42	45.2	341	1	MURB_HABIN	P44605_haemophilus	220	41	44.1	448	2	096208_PLAF7	096208_plasmodium
148	42	45.2	343	2	042654_CHRAE	042654_chrysosplen	221	41	44.1	448	2	03VUR2_9CHLB	03VUR2_pelodictyon
149	42	45.2	350	2	03F512_9BORR	03F512_burkholderi	222	41	44.1	458	2	044KV3_CHRSL	044KV3_chromohalob
150	42	45.2	351	2	044VDE_9BURK	044VDE_burkholderi	223	41	44.1	476	2	04WU22_ASPPU	04WU22_aspergillus
151	42	45.2	351	2	04LPD2_BURVI	04LPD2_burkholderi	224	41	44.1	506	2	08MCQ3_9FABA	08MCQ3_medicago pl
152	42	45.2	351	2	04LXDO_9BURK	04LXDO_burkholderi	225	41	44.1	566	1	HCYB_PONLE	HCYB_pontastacus
153	42	45.2	351	2	039FK9_BURS3	039FK9_burkholderi	226	41	44.1	650	1	HCYB_CARAE	HCYB_carolinus ae
154	42	45.2	385	2	05E5P0_VIBFI	05E5P0_vibrio fusc	227	41	44.1	657	1	HCYB_PANIN	HCYB_penillius i
155	42	45.2	394	2	03QZP9_XYLFA	03QZP9_xyloella fas	228	41	44.1	657	2	070E44_ANOGA	070E44_anopheles g
156	42	45.2	394	2	03RDT1_XYLFA	03RDT1_xyloella fas	229	41	44.1	659	2	HCYB_SCUCO	HCYB_scutigera c
157	42	45.2	418	2	P73784_SYNY3	P73784_synochocycr	230	41	44.1	662	2	05G2A8_CANNM	05G2A8_cancer magi
158	42	45.2	423	1	YHUV_ECOLI	P37660_escherichia	231	41	44.1	662	2	05G2A7_CANNM	05G2A7_cancer magi
159	42	45.2	423	2	031V66_SHIBS	031V66_shigella bo	232	41	44.1	663	2	05G2A6_CANNM	05G2A6_cancer magi
160	42	45.2	423	2	03YV80_SHIBS	03YV80_shigella bo	233	41	44.1	669	2	09NRY6_PENYA	09NRY6_penaeus van
161	42	45.2	423	2	02M7K1_ECOLI	02M7K1_escherichia	234	41	44.1	671	2	05G2A5_CANNM	05G2A5_cancer magi
162	42	45.2	423	2	083P82_SHIFL	083P82_shigella fl	235	41	44.1	676	2	023707_CANNM	023707_cancer magi
163	42	45.2	526	2	07V2D6_PROMP	07V2D6_pirochlocco	236	41	44.1	676	2	05G2A4_CANNM	05G2A4_cancer magi
164	42	45.2	556	2	05V0X8_HALMA	05V0X8_haloarcula	237	41	44.1	676	2	09NGJ5_CALST	09NGJ5_callicectes
165	42	45.2	625	2	086N91_9ARAC	086N91_nephila ina	238	41	44.1	680	2	089UJ2_BRAVA	089UJ2_bradynothob
166	42	45.2	638	2	04CAY6_CROWT	04CAY6_crocophaner	239	41	44.1	684	2	09SP18_PALUV	09SP18_pallinurus v
167	42	45.2	670	2	025271_LEPDE	025271_leptinotars	240	41	44.1	684	2	09SP19_PALUV	09SP19_pallinurus v
168	42	45.2	685	2	07P6P1_ANOGA	07P6P1_anopheles g	241	41	44.1	684	2	081F75_9EUCU	081F75_pallinurus v
169	42	45.2	685	2	08WMZ2_ANOGA	08WMZ2_anopheles g	242	41	44.1	685	2	09SP17_PALUV	09SP17_pallinurus v
170	42	45.2	685	2	09GU89_BOWMO	09GU89_bombyx mori	243	41	44.1	685	2	06Y021_PACLE	06Y021_pacificastacu
171	42	45.2	686	2	044251_ANOGA	044251_anopheles g	244	41	44.1	687	2	04QAS4_LEIMA	04QAS4_leishmania
172	42	45.2	686	2	096453_ANOST	096453_anopheles g	245	41	44.1	688	2	09Y0B3_SARBU	09Y0B3_sarcophaga
173	42	45.2	686	2	07P6P3_ANOGA	07P6P3_anopheles g	246	41	44.1	691	2	06L466_SOLDE	06L466_solanum dem
174	42	45.2	687	2	086R06_9DIPT	086R06_anopheles c	247	41	44.1	744	2	09U5Y8_9HYWE	09U5Y8_campocetus
175	42	45.2	687	2	096753_ANOGA	096753_anopheles g	248	41	44.1	750	2	077065_CHOPU	077065_choristoneu
176	42	45.2	687	2	07P100_ANOGA	07P100_anopheles g	249	41	44.1	753	2	09Y1W5_TENNO	09Y1W5_tenebrio mo
177	42	45.2	690	2	027598_DROME	027598_drosophila	250	41	44.1	754	2		



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OM protein - protein search, using SW model

Run on: August 9, 2006, 15:36:13 / Search time 39 Seconds  
(without alignments)  
41.941 Million cell updates/sec

Title: US-10-810-919-4

Perfect score: 93

Sequence: 1 VHHQKLPPFADVGSNK 17

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	90.3	42	2	PN0512
2	84	90.3	57	2	A60045
3	84	90.3	57	2	F60045
4	84	90.3	57	2	D60045
5	84	90.3	57	2	E60045
6	84	90.3	57	2	G60045
7	84	90.3	57	2	B60045
8	84	90.3	82	2	P00438
9	84	90.3	695	1	A49795
10	84	90.3	770	1	QRH04
11	80	86.0	747	2	JH0773
12	76	81.7	33	2	S23094
13	76	81.7	695	2	A27485
14	76	81.7	695	2	S00550
15	48	51.6	477	2	T47753
16	45	48.4	279	2	F84112
17	44	47.3	624	1	BHRL
18	44	47.3	704	2	A34287
19	43	46.2	251	2	C71879
20	43	46.2	703	2	B34434
21	42	46.2	341	1	A82089
22	42	45.2	341	1	G64058
23	42	45.2	418	2	S74875
24	42	45.2	423	2	S47761
25	42	45.2	649	2	S58064
26	41	44.1	240	1	Z1ZMD1
27	41	44.1	259	2	T22775
28	41	44.1	320	2	C83628
29	41	44.1	380	2	JQ2338

30	41	44.1	390	2	D83853	cystathionine beta
31	41	44.1	447	2	D71611	hypothetical prote
32	41	44.1	657	1	BHLOA	hemocyanin chain a
33	41	44.1	657	1	BHLOA	hemocyanin chain b
34	40	43.0	220	2	A12182	hypothetical prote
35	40	43.0	297	2	E56273	sapa 5'-region hyp
36	40	43.0	302	2	S37579	probable transpos
37	40	43.0	336	2	T38902	probable cinamo
38	40	43.0	423	2	G86027	probable transport
39	40	43.0	423	2	C91181	probable transport
40	40	43.0	491	2	D84967	glucose-6-phosphat
41	40	43.0	491	2	AB0742	glucose-6-phosphat
42	40	43.0	513	2	T01413	probable histone d
43	40	43.0	626	2	S67964	hemocyanin chain 6
44	40	43.0	631	1	BHRLA	hemocyanin chain a
45	40	43.0	662	2	S5387	hemocyanin precurs
46	40	43.0	672	2	JC7676	hemocyanin A precu
47	40	43.0	699	2	H64118	4-alpha-glucanot
48	40	43.0	702	2	C86268	F1384.2 protein -
49	40	43.0	992	1	GNMVR3	structural polypro
50	40	43.0	1063	1	GNMVR7	structural polypro
51	40	43.0	1063	1	GNMVR4	structural polypro
52	40	43.0	1063	1	GNMVR4	structural polypro
53	39.5	42.5	493	2	S68430	guanine tRNA-ribos
54	39.5	42.5	494	2	G01932	guanine tRNA-ribos
55	39	41.9	292	2	D81140	5,10-methylentetr
56	39	41.9	292	2	F81880	probable 5,10-meth
57	39	41.9	313	2	C83874	arsenical pump-drt
58	39	41.9	334	2	JC4681	bradykinin B1 rece
59	39	41.9	357	2	S75666	3-chlorobenzoate-3
60	39	41.9	382	2	B86268	F1384.1 protein -
61	39	41.9	394	2	D87225	nicotinate phospho
62	39	41.9	435	2	T33324	probable JNK-activ
63	39	41.9	435	2	AC0104	probable sugar tra
64	39	41.9	448	2	T16256	hypothetical prote
65	39	41.9	455	2	T50426	hypothetical prote
66	39	41.9	565	2	T29813	hypothetical prote
67	39	41.9	661	2	S21221	hemocyanin chain c
68	39	41.9	683	1	A23690	protein kinase (EC
69	39	41.9	683	1	S29478	protein kinase C (
70	39	41.9	723	1	S46744	P1P1 protein homol
71	39	41.9	900	1	S25322	bifunctional beta-
72	39	41.9	1299	2	T24299	hypothetical prote
73	39	41.9	2374	2	T21052	hypothetical prote
74	38	40.9	202	2	B82386	malate synthase-re
75	38	40.9	273	2	D82208	conserved hypothet
76	38	40.9	311	2	G68324	hypothetical prote
77	38	40.9	319	2	H90055	hypothetical prote
78	38	40.9	354	2	G96795	hypothetical prote
79	38	40.9	367	2	A81180	B. subtilis yxjH a
80	38	40.9	367	2	A81180	B. subtilis yxjH a
81	38	40.9	390	2	C75103	na+/h+ antiporter
82	38	40.9	491	2	S37053	glucose-6-phosphat
83	38	40.9	535	2	S15777	transposase - rice
84	38	40.9	641	2	A55549	glucan 1,6-alpha-i
85	38	40.9	667	2	C69723	transketolase (EC
86	38	40.9	682	1	A39666	protein kinase C (
87	38	40.9	713	1	H97827	organic solvent to
88	38	40.9	736	1	KIRBCE	protein kinase C (
89	38	40.9	737	1	KIRBCE	protein kinase C (
90	38	40.9	737	1	KIRBCE	protein kinase C (
91	38	40.9	737	1	S28942	protein kinase C (
92	38	40.9	875	2	A53901	ribonuclease P (EC
93	38	40.9	1026	2	B66663	hypothetical prote
94	38	40.9	1146	2	C83304	hypothetical prote
95	38	40.9	1231	2	T24435	hypothetical prote
96	38	40.9	1238	2	T15824	hypothetical prote
97	38	40.9	1377	2	A38926	DNA-binding protei
98	37.5	40.3	225	2	B5387	hypothetical prote
99	37.5	40.3	336	2	B82064	fructose-1,6-bisph
100	37.5	40.3	409	2	S72438	phosphatidyleth
101	37	39.8	130	2	B89793	hypothetical prote
102	37	39.8	166	2	A97174	chemotaxis protein

103	37	39.8	173	2	D86825	pyrimidine operon
104	37	39.8	175	2	A89892	pyrimidine operon
105	37	39.8	175	2	F82486	conserved hypotet
106	37	39.8	178	2	D97160	uracil phosphoribo
107	37	39.8	179	1	G64069	uracil phosphoribo
108	37	39.8	179	1	S38992	uracil phosphoribo
109	37	39.8	183	2	E75435	pyrimidine operon
110	37	39.8	183	2	AH1304	pyrimidine operon
111	37	39.8	183	2	AH1676	pyrimidine operon
112	37	39.8	183	2	H87707	alkyl hydoperoxid
113	37	39.8	193	2	H70958	probable uracil ph
114	37	39.8	199	2	S26047	transformer sex-de
115	37	39.8	240	2	C87409	hypothetical prote
116	37	39.8	247	2	H69827	conserved hypotet
117	37	39.8	255	2	S41511	Brn-3a protein - m
118	37	39.8	263	2	I40199	transposase - Bact
119	37	39.8	276	2	C64417	hypothetical prote
120	37	39.8	296	2	I46021	Fc-gamma receptor
121	37	39.8	301	2	P00162	arylphorin (clone
122	37	39.8	306	2	G69674	beta-lactamase (EC
123	37	39.8	349	2	T31788	hypothetical prote
124	37	39.8	351	2	S76925	hypothetical prote
125	37	39.8	371	2	AH0686	hypothetical prote
126	37	39.8	381	2	P84107	glycosyltransferas
127	37	39.8	387	2	G70398	1,3 propenediol de
128	37	39.8	419	1	E5ECRM	erythromycin ester
129	37	39.8	424	1	AB0289	tyrosine-tRNA liga
130	37	39.8	430	1	E69659	molybdopterin bios
131	37	39.8	447	2	T00425	photoiyase/blue-11
132	37	39.8	475	2	AC1926	hypothetical prote
133	37	39.8	485	2	E70363	4-alpha-glucanotra
134	37	39.8	494	2	AB0252	glucose-6-phosphat
135	37	39.8	499	2	E82977	glycolate oxidase
136	37	39.8	502	2	AH2289	4-alpha-glucanotra
137	37	39.8	502	2	E71963	probable cardiolip
138	37	39.8	502	2	P64543	conserved hypotet
139	37	39.8	533	2	S43142	sucrose transport
140	37	39.8	537	2	AE2454	two-component sens
141	37	39.8	548	2	S37969	probable triacylg1
142	37	39.8	632	2	I51682	epithelial sodium
143	37	39.8	687	2	J01044	arylphorin precurs
144	37	39.8	748	2	B45046	basic juvenile hor
145	37	39.8	759	2	U01045	arylphorin precurs
146	37	39.8	832	2	H71916	DNA mismatch repai
147	37	39.8	862	2	H84848	phospholipase D [i
148	37	39.8	1341	2	T18301	lactophillin-2, spl
149	37	39.8	1354	2	T18375	lactophillin-2, spl
150	37	39.8	1356	2	T18367	lactophillin-2, spl
151	37	39.8	1369	2	T18379	lactophillin-2, spl
152	37	39.8	1375	2	T30813	plasmidogen relate
153	37	39.8	1384	2	T18366	lactophillin-2, spl
154	37	39.8	1397	2	T18377	lactophillin-2, spl
155	37	39.8	1399	2	T18370	lactophillin-2, spl
156	37	39.8	1407	2	T18381	lactophillin-2, spl
157	37	39.8	1412	2	T18380	lactophillin-2, spl
158	37	39.8	1420	2	T18383	lactophillin-2, spl
159	37	39.8	1422	2	T18385	lactophillin-2, spl
160	37	39.8	1435	2	T18387	lactophillin-2, spl
161	37	39.8	1450	2	T18382	lactophillin-2, spl
162	37	39.8	1463	2	T18386	lactophillin-2, spl
163	37	39.8	1478	2	T18384	lactophillin-2, spl
164	37	39.8	1478	2	T18388	lactophillin-2, spl
165	37	39.8	2150	1	S27802	zinc finger protei
166	37	39.8	2150	1	T19450	hypothetical prote
167	37	39.8	3135	2	A48584	transmission block
168	37	39.8	329	1	A32541	histatin 1 precurs
169	36.5	39.2	153	2	UC4359	nucleoside-diphosp
170	36.5	39.2	195	2	A99240	anthranilate synth
171	36.5	39.2	195	2	B40635	anthranilate synth
172	36.5	39.2	284	2	A12008	formyltetrahydrofo
173	36.5	39.2	297	2	AF1618	endonuclease IV ho
174	36.5	39.2	371	2	T08485	kIbB protein - Bnt
175	36.5	39.2	551	2	P70111	V-type ATPase, sub
176	36.5	39.2	2628	2	S59413	probable membrane
177	36	38.7	98	2	JC5064	S-100 calcium-bind
178	36	38.7	98	2	JC5065	calcium-binding pr
179	36	38.7	109	2	C64402	hypothetical prote
180	36	38.7	134	2	F64861	YcgX protein - Bsc
181	36	38.7	142	2	T45922	probable C2H2-type
182	36	38.7	151	2	A86695	hypothetical prote
183	36	38.7	179	2	G87439	conserved hypotet
184	36	38.7	181	1	B57986	uracil phosphoribo
185	36	38.7	225	2	C70045	conserved hypotet
186	36	38.7	235	2	AG3072	two-component resp
187	36	38.7	235	2	B98214	conserved hypotet
188	36	38.7	245	2	JE0179	bai1 protein (Ari7
189	36	38.7	255	2	T22863	protein-glutamine
190	36	38.7	276	1	BVBCG	hypothetical prote
191	36	38.7	276	1	D86008	glip protein - Bsc
192	36	38.7	276	1	C91162	protein of gip reg
193	36	38.7	284	2	C83237	probable transcrip
194	36	38.7	289	2	B64330	dihydrodipicolinat
195	36	38.7	308	2	D81297	probable belenide,
196	36	38.7	312	2	T27004	hypothetical prote
197	36	38.7	315	2	F90589	conserved hypotet
198	36	38.7	331	2	E83368	conserved hypotet
199	36	38.7	342	2	AF1203	transcription regu
200	36	38.7	348	2	T13320	hypothetical prote
201	36	38.7	348	2	T13625	hypothetical prote
202	36	38.7	348	2	A56197	nuclear hormone re
203	36	38.7	360	2	F70045	two-component sens
204	36	38.7	360	2	JE0116	zinc-finger protei
205	36	38.7	362	2	AF0159	probable membrane
206	36	38.7	365	2	C64309	hypothetical prote
207	36	38.7	368	2	A11934	hypothetical prote
208	36	38.7	371	2	B84113	response regulator
209	36	38.7	378	2	B84714	probable ARP2/3 pr
210	36	38.7	378	2	A84719	probable ARP2/3 pr
211	36	38.7	400	2	D64462	hypothetical prote
212	36	38.7	420	2	C87790	protein B0207.3 [i
213	36	38.7	434	2	T04471	probable 4-hydroxy
214	36	38.7	453	2	A95212	anthranilate synth
215	36	38.7	456	2	B96688	unknown protein, 1
216	36	38.7	458	2	C82952	ATP synthase beta
217	36	38.7	458	2	T33814	hypothetical prote
218	36	38.7	467	2	S61105	hypothetical prote
219	36	38.7	467	2	E87566	hypothetical prote
220	36	38.7	486	2	C98076	anthranilate synth
221	36	38.7	491	1	D64947	glucose-6-phosphat
222	36	38.7	491	2	F85797	glucose-6-phosphat
223	36	38.7	491	2	B90949	glucose-6-phosphat
224	36	38.7	491	2	E96691	probable sucrose-p
225	36	38.7	492	2	A84520	probable sucrose-p
226	36	38.7	499	2	S74396	hypothetical prote
227	36	38.7	499	2	C70405	hypothetical prote
228	36	38.7	503	2	A12342	hypothetical prote
229	36	38.7	523	2	T40370	dhna-(apurinic or a
230	36	38.7	527	2	T22867	hypothetical prote
231	36	38.7	550	1	A48026	sterol-O-acyltans
232	36	38.7	580	2	T40867	aspartate-tRNA lig
233	36	38.7	586	2	S66697	probable membrane
234	36	38.7	592	2	T15413	hypothetical prote
235	36	38.7	669	2	A49585	Na+ channel protei
236	36	38.7	699	2	S29489	sodium channel pro
237	36	38.7	702	2	A34434	arylphorin alpha c
238	36	38.7	776	1	H69430	probable formate C
239	36	38.7	833	2	T01547	probable phosphol
240	36	38.7	880	2	S50801	AMP deaminase homo
241	36	38.7	998	2	T03784	probable receptor
242	36	38.7	1235	1	TNB396	hypothetical prote
243	36	38.7	1314	1	T18961	transcription regu
244	36	38.7	1375	1	T18961	FBI protein homol
245	36	38.7	1751	1	MMHDMH	laminin alpha-2 ch
246	36	38.7	3375	1	T19821	hypothetical prote
247	35.5	38.2	114	2	S09752	hypothetical prote
248	35.5	38.2	274	2	F81350	formyltetrahydrofo

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OM protein - protein search, using sw model

Run on: August 9, 2006, 15:31:47 ; Search time 194 Seconds  
(without alignments)  
40.065 Million cell updates/sec

Title: US-10-810-919-4  
Perfect score: 93  
Sequence: 1 VHQKLPFFADVGSNK 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :

- 1: A\_genseq\_8:\*
- 2: geneeqp1980s:\*
- 3: geneeqp1990s:\*
- 4: geneeqp2000s:\*
- 5: geneeqp2001s:\*
- 6: geneeqp2002s:\*
- 7: geneeqp2003as:\*
- 8: geneeqp2004s:\*
- 9: geneeqp2005s:\*
- 10: geneeqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	100.0	17	8	ADSI18448
2	84	90.3	17	2	AAR54703
3	84	90.3	17	4	AAB91774
4	84	90.3	17	4	AAB91807
5	84	90.3	17	5	ABBO4911
6	84	90.3	17	6	ABBO4911
7	84	90.3	17	8	ADCS3165
8	84	90.3	17	8	ADCS3165
9	84	90.3	17	8	ADCS3165
10	84	90.3	17	8	ADCS3165
11	84	90.3	17	8	ADCS3165
12	84	90.3	17	8	ADCS3165
13	84	90.3	17	8	ADCS3165
14	84	90.3	17	8	ADCS3165
15	84	90.3	17	8	ADCS3165
16	84	90.3	17	8	ADCS3165
17	84	90.3	17	8	ADCS3165
18	84	90.3	17	8	ADCS3165
19	84	90.3	17	8	ADCS3165
20	84	90.3	17	8	ADCS3165
21	84	90.3	17	8	ADCS3165
22	84	90.3	17	8	ADCS3165
23	84	90.3	17	8	ADCS3165

24	84	90.3	28	2	AAW01413	AAW01413	Beta/A4-a
25	84	90.3	28	2	AAV39805	AAV39805	Beta-amy1
26	84	90.3	28	2	AAW81467	AAW81467	Synthetic
27	84	90.3	28	4	AAW35591	AAW35591	Human c10
28	84	90.3	28	4	AAW35595	AAW35595	Human c10
29	84	90.3	28	4	AAW35594	AAW35594	Human c10
30	84	90.3	28	4	AAW35592	AAW35592	Human c10
31	84	90.3	28	4	AAW35593	AAW35593	Human c10
32	84	90.3	28	4	AAW35596	AAW35596	Human c10
33	84	90.3	28	4	AAW35590	AAW35590	Human c10
34	84	90.3	28	4	AAW35591	AAW35591	Human c10
35	84	90.3	28	4	AAW35592	AAW35592	Human c10
36	84	90.3	28	4	AAW35593	AAW35593	Human c10
37	84	90.3	28	4	AAW35594	AAW35594	Human c10
38	84	90.3	28	4	AAW35595	AAW35595	Human c10
39	84	90.3	28	4	AAW35596	AAW35596	Human c10
40	84	90.3	28	4	AAW35597	AAW35597	Human c10
41	84	90.3	28	4	AAW35598	AAW35598	Human c10
42	84	90.3	28	4	AAW35599	AAW35599	Human c10
43	84	90.3	28	4	AAW35600	AAW35600	Human c10
44	84	90.3	28	4	AAW35601	AAW35601	Human c10
45	84	90.3	28	4	AAW35602	AAW35602	Human c10
46	84	90.3	28	4	AAW35603	AAW35603	Human c10
47	84	90.3	28	4	AAW35604	AAW35604	Human c10
48	84	90.3	28	4	AAW35605	AAW35605	Human c10
49	84	90.3	28	4	AAW35606	AAW35606	Human c10
50	84	90.3	28	4	AAW35607	AAW35607	Human c10
51	84	90.3	28	4	AAW35608	AAW35608	Human c10
52	84	90.3	28	4	AAW35609	AAW35609	Human c10
53	84	90.3	28	4	AAW35610	AAW35610	Human c10
54	84	90.3	28	4	AAW35611	AAW35611	Human c10
55	84	90.3	28	4	AAW35612	AAW35612	Human c10
56	84	90.3	28	4	AAW35613	AAW35613	Human c10
57	84	90.3	28	4	AAW35614	AAW35614	Human c10
58	84	90.3	28	4	AAW35615	AAW35615	Human c10
59	84	90.3	28	4	AAW35616	AAW35616	Human c10
60	84	90.3	28	4	AAW35617	AAW35617	Human c10
61	84	90.3	28	4	AAW35618	AAW35618	Human c10
62	84	90.3	28	4	AAW35619	AAW35619	Human c10
63	84	90.3	28	4	AAW35620	AAW35620	Human c10
64	84	90.3	28	4	AAW35621	AAW35621	Human c10
65	84	90.3	28	4	AAW35622	AAW35622	Human c10
66	84	90.3	28	4	AAW35623	AAW35623	Human c10
67	84	90.3	28	4	AAW35624	AAW35624	Human c10
68	84	90.3	28	4	AAW35625	AAW35625	Human c10
69	84	90.3	28	4	AAW35626	AAW35626	Human c10
70	84	90.3	28	4	AAW35627	AAW35627	Human c10
71	84	90.3	28	4	AAW35628	AAW35628	Human c10
72	84	90.3	28	4	AAW35629	AAW35629	Human c10
73	84	90.3	28	4	AAW35630	AAW35630	Human c10
74	84	90.3	28	4	AAW35631	AAW35631	Human c10
75	84	90.3	28	4	AAW35632	AAW35632	Human c10
76	84	90.3	28	4	AAW35633	AAW35633	Human c10
77	84	90.3	28	4	AAW35634	AAW35634	Human c10
78	84	90.3	28	4	AAW35635	AAW35635	Human c10
79	84	90.3	28	4	AAW35636	AAW35636	Human c10
80	84	90.3	28	4	AAW35637	AAW35637	Human c10
81	84	90.3	28	4	AAW35638	AAW35638	Human c10
82	84	90.3	28	4	AAW35639	AAW35639	Human c10
83	84	90.3	28	4	AAW35640	AAW35640	Human c10
84	84	90.3	28	4	AAW35641	AAW35641	Human c10
85	84	90.3	28	4	AAW35642	AAW35642	Human c10
86	84	90.3	28	4	AAW35643	AAW35643	Human c10
87	84	90.3	28	4	AAW35644	AAW35644	Human c10
88	84	90.3	28	4	AAW35645	AAW35645	Human c10
89	84	90.3	28	4	AAW35646	AAW35646	Human c10
90	84	90.3	28	4	AAW35647	AAW35647	Human c10
91	84	90.3	28	4	AAW35648	AAW35648	Human c10
92	84	90.3	28	4	AAW35649	AAW35649	Human c10
93	84	90.3	28	4	AAW35650	AAW35650	Human c10
94	84	90.3	28	4	AAW35651	AAW35651	Human c10
95	84	90.3	28	4	AAW35652	AAW35652	Human c10
96	84	90.3	28	4	AAW35653	AAW35653	Human c10

97	84	90.3	36	6	ABR42774	Abv42774	Amyloid b	170	84	90.3	40	7	ADF55648	Adf55648	Human A b
98	84	90.3	36	8	ADP73823	ADP73823	Loop Inse	171	84	90.3	40	7	ADK82702	Adk82702	Beta-amy1
99	84	90.3	36	9	AED47512	Aed47512	Beta secr	172	84	90.3	40	8	ADF53270	Adf53270	Amyloid A
100	84	90.3	36	10	AEE39871	Aee39871	Amyloidge	173	84	90.3	40	8	ADN00693	Adn00693	A40, SEQ
101	84	90.3	38	2	AAR60362	Aar60362	Beta-amy1	174	84	90.3	40	8	ADN41885	Adn41885	Amino aci
102	84	90.3	38	2	AAW92722	Aaw92722	Human tac	175	84	90.3	40	8	ADN41881	Adn41881	Amino aci
103	84	90.3	38	4	AAAB91826	Aab91826	Amyloid b	176	84	90.3	40	8	ADN41882	Adn41882	Amino aci
104	84	90.3	38	4	AAAB91799	Aab91799	Amyloid b	177	84	90.3	40	8	ADN41884	Adn41884	Amino aci
105	84	90.3	38	4	ADU24436	Adu24436	Novel glu	178	84	90.3	40	8	ADN41865	Adn41865	Amino aci
106	84	90.3	38	8	ADU24441	Adu24441	Novel glu	179	84	90.3	40	8	ADN41880	Adn41880	Amino aci
107	84	90.3	38	8	ADU46715	Adu46715	Gln3 amy1	180	84	90.3	40	8	ADN41880	Adn41880	Amino aci
108	84	90.3	38	8	ADU46710	Adu46710	Amyloid b	181	84	90.3	40	8	ADQ37253	Adq37253	Human amy
109	84	90.3	38	9	ADY81762	Ady81762	Human bet	182	84	90.3	40	8	ADQ37253	Adq37253	Vaccine a
110	84	90.3	38	9	ADZ71362	Adz71362	Human bet	183	84	90.3	40	8	ADP16410	Adp16410	Human Abe
111	84	90.3	38	9	ADZ71367	Adz71367	Human bet	184	84	90.3	40	8	ADP18445	Adp18445	Amyloid b
112	84	90.3	38	9	AEA35400	Aea35400	Novel QC	185	84	90.3	40	8	ADU20812	Adu20812	Amyloid b
113	84	90.3	38	9	AEA35395	Aea35395	Novel QC	186	84	90.3	40	8	ADU24435	Adu24435	Novel glu
114	84	90.3	38	9	AEB92568	Aeb92568	Glutamy	187	84	90.3	40	8	ADU24434	Adu24434	Novel glu
115	84	90.3	38	9	AEB92573	Aeb92573	Glutamy	188	84	90.3	40	8	ADU46709	Adu46709	Amyloid b
116	84	90.3	38	10	AEB39872	Aeb39872	Amyloidge	189	84	90.3	40	8	ADU46708	Adu46708	Amyloid b
117	84	90.3	39	2	AAR60363	Aar60363	Beta-amy1	190	84	90.3	40	9	ADV50921	Adv50921	Alzheimer
118	84	90.3	39	2	AAW81472	Aaw81472	Synthetic	191	84	90.3	40	9	ADW38388	Adw38388	Human bet
119	84	90.3	39	2	AAV25134	Aav25134	Human amy	192	84	90.3	40	9	ADY72249	Ady72249	N-termina
120	84	90.3	39	3	AAV52132	Aav52132	Human Rec	193	84	90.3	40	9	ADY81764	Ady81764	Human bet
121	84	90.3	39	6	AEU08509	Aeu08509	Human amy	194	84	90.3	40	9	ADY78385	Ady78385	Human amy
122	84	90.3	39	6	ABP96148	Abp96148	Human Abe	195	84	90.3	40	9	ADZ20480	Adz20480	Amyloid b
123	84	90.3	39	6	ADY81763	Ady81763	Human bet	196	84	90.3	40	9	ADZ59193	Adz59193	Human amy
124	84	90.3	39	10	AEP87774	Aep87774	Human bet	197	84	90.3	40	9	ADZ71361	Adz71361	Human bet
125	84	90.3	40	2	AAR33191	Aar33191	Beta-amy1	198	84	90.3	40	9	ADZ71360	Adz71360	Human bet
126	84	90.3	40	2	AAR60364	Aar60364	Beta-amy1	199	84	90.3	40	9	AEA35393	Aea35393	Novel QC
127	84	90.3	40	2	ADD11651	Add11651	Human bet	200	84	90.3	40	9	AEA35394	Aea35394	Novel QC
128	84	90.3	40	2	AAW23335	Aaw23335	Amyloid b	201	84	90.3	40	9	AEB09193	Aeb09193	Human bet
129	84	90.3	40	2	AAW37507	Aaw37507	Amyloid b	202	84	90.3	40	9	AEB88137	Aeb88137	Human nep
130	84	90.3	40	2	AAW47226	Aaw47226	Beta-amy1	203	84	90.3	40	9	AEB92567	Aeb92567	Glutamy
131	84	90.3	40	2	AAW14099	Aaw14099	Human bet	204	84	90.3	40	9	AEB92567	Aeb92567	Glutamy
132	84	90.3	40	2	AAV39804	Aav39804	Beta-amy1	205	84	90.3	40	9	AEC05253	Aec05253	Amyloid b
133	84	90.3	40	2	AAW95854	Aaw95854	Wild type	206	84	90.3	40	9	AEC39344	Aec39344	Amyloid b
134	84	90.3	40	2	AAW81473	Aaw81473	Synthetic	207	84	90.3	40	9	AED21140	Aed21140	Amyloid b
135	84	90.3	40	2	AAV39339	Aav39339	Beta-amy1	208	84	90.3	40	9	AED33058	Aed33058	Human amy
136	84	90.3	40	2	AAV25135	Aav25135	Human amy	209	84	90.3	40	10	AEB92546	Aeb92546	Amyloid b
137	84	90.3	40	2	AAW92723	Aaw92723	Human tac	210	84	90.3	40	10	AEB92546	Aeb92546	Human amy
138	84	90.3	40	2	AAW84426	Aaw84426	Partial s	211	84	90.3	40	10	AEB92546	Aeb92546	Human amy
139	84	90.3	40	4	AAW84429	Aaw84429	Partial s	212	84	90.3	40	10	AEB92546	Aeb92546	Human amy
140	84	90.3	40	4	AAW91813	Aaw91813	Amyloid b	213	84	90.3	40	10	AEB92546	Aeb92546	Human amy
141	84	90.3	40	4	AAW91780	Aaw91780	Amyloid b	214	84	90.3	40	10	AEB92546	Aeb92546	Human amy
142	84	90.3	40	4	AAW91829	Aaw91829	Amyloid b	215	84	90.3	40	10	AEB92546	Aeb92546	Human amy
143	84	90.3	40	4	AAW91802	Aaw91802	Amyloid b	216	84	90.3	40	10	AEB92546	Aeb92546	Human amy
144	84	90.3	40	4	AAW94425	Aaw94425	Human pep	217	84	90.3	40	10	AEB92546	Aeb92546	Human amy
145	84	90.3	40	5	AAE22990	Aae22990	Human amy	218	84	90.3	40	10	AEB92546	Aeb92546	Human amy
146	84	90.3	40	5	AAE22990	Aae22990	Human amy	219	84	90.3	40	10	AEB92546	Aeb92546	Human amy
147	84	90.3	40	5	AAU11773	Aau11773	Synthetic	220	84	90.3	40	10	AEB92546	Aeb92546	Human amy
148	84	90.3	40	5	AAU11772	Aau11772	Synthetic	221	84	90.3	40	10	AEB92546	Aeb92546	Human amy
149	84	90.3	40	5	AAU68313	Aau68313	Human bet	222	84	90.3	40	10	AEB92546	Aeb92546	Human amy
150	84	90.3	40	5	AAU96895	Aau96895	Human bet	223	84	90.3	40	10	AEB92546	Aeb92546	Human amy
151	84	90.3	40	5	AAU96895	Aau96895	Human bet	224	84	90.3	40	10	AEB92546	Aeb92546	Human amy
152	84	90.3	40	5	AAU96895	Aau96895	Human bet	225	84	90.3	40	10	AEB92546	Aeb92546	Human amy
153	84	90.3	40	5	AAU96895	Aau96895	Human bet	226	84	90.3	40	10	AEB92546	Aeb92546	Human amy
154	84	90.3	40	5	AAU96895	Aau96895	Human bet	227	84	90.3	40	10	AEB92546	Aeb92546	Human amy
155	84	90.3	40	5	AAU96895	Aau96895	Human bet	228	84	90.3	40	10	AEB92546	Aeb92546	Human amy
156	84	90.3	40	5	AAU96895	Aau96895	Human bet	229	84	90.3	40	10	AEB92546	Aeb92546	Human amy
157	84	90.3	40	5	AAU96895	Aau96895	Human bet	230	84	90.3	40	10	AEB92546	Aeb92546	Human amy
158	84	90.3	40	5	AAU96895	Aau96895	Human bet	231	84	90.3	40	10	AEB92546	Aeb92546	Human amy
159	84	90.3	40	5	AAU96895	Aau96895	Human bet	232	84	90.3	40	10	AEB92546	Aeb92546	Human amy
160	84	90.3	40	5	AAU96895	Aau96895	Human bet	233	84	90.3	40	10	AEB92546	Aeb92546	Human amy
161	84	90.3	40	5	AAU96895	Aau96895	Human bet	234	84	90.3	40	10	AEB92546	Aeb92546	Human amy
162	84	90.3	40	5	AAU96895	Aau96895	Human bet	235	84	90.3	40	10	AEB92546	Aeb92546	Human amy
163	84	90.3	40	5	AAU96895	Aau96895	Human bet	236	84	90.3	40	10	AEB92546	Aeb92546	Human amy
164	84	90.3	40	5	AAU96895	Aau96895	Human bet	237	84	90.3	40	10	AEB92546	Aeb92546	Human amy
165	84	90.3	40	5	AAU96895	Aau96895	Human bet	238	84	90.3	40	10	AEB92546	Aeb92546	Human amy
166	84	90.3	40	5	AAU96895	Aau96895	Human bet	239	84	90.3	40	10	AEB92546	Aeb92546	Human amy
167	84	90.3	40	5	AAU96895	Aau96895	Human bet	240	84	90.3	40	10	AEB92546	Aeb92546	Human amy
168	84	90.3	40	5	AAU96895	Aau96895	Human bet	241	84	90.3	40	10	AEB92546	Aeb92546	Human amy
169	84	90.3	40	5	AAU96895	Aau96895	Human bet	242	84	90.3	40	10	AEB92546	Aeb92546	Human amy